

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/526,062  
Source: PG/10  
Date Processed by STIC: 3/9/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/09/2005

PATENT APPLICATION: US/10/526,062

TIME: 15:16:31

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\03092005\J526062.raw

4 <110> APPLICANT: Biemans, Ralph  
 5 Denoel, Philippe  
 6 Feron, Christiane  
 7 Goraj, Karine  
 8 Kortekaas, Jeroen  
 9 Poolman, Jan  
 10 Tommassen, Jan  
 11 Weynants, Vincent  
 14 <120> TITLE OF INVENTION: Mutant Protein and Refolding Method  
 17 <130> FILE REFERENCE: VB60394  
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/526,062  
 20 <141> CURRENT FILING DATE: 2005-02-28  
 22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/009634  
 23 <151> PRIOR FILING DATE: 2003-08-28  
 25 <150> PRIOR APPLICATION NUMBER: GB 0220199.4  
 26 <151> PRIOR FILING DATE: 2002-08-30  
 28 <160> NUMBER OF SEQ ID NOS: 31  
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 33 <211> LENGTH: 28  
 34 <212> TYPE: PRT  
 35 <213> ORGANISM: Neisseria meningitidis  
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 39 1 5 10 15  
 40 Gln Met Lys Asp Arg Ala Asp Glu Asp Thr Val His  
 41 20 25  
 44 <210> SEQ ID NO: 2  
 45 <211> LENGTH: 24  
 46 <212> TYPE: PRT  
 47 <213> ORGANISM: Neisseria meningitidis  
 49 <400> SEQUENCE: 2  
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 51 1 5 10 15  
 52 Lys Ser Ser Arg Ile Asn Ile Asp  
 53 20  
 56 <210> SEQ ID NO: 3  
 57 <211> LENGTH: 2307  
 58 <212> TYPE: DNA  
 59 <213> ORGANISM: Neisseria meningitidis  
 61 <400> SEQUENCE: 3  
 62 tggttaataataataaaata attattaatt atttttctta tcctgccaaa tcttaacggt 60  
 63 ttggatttac ttcccttcat actcaagagg acgattgaat gaatacccca ttgttccgctc 120

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64 tcagcctgct ctcgctcaca cttgcggcag gttttgcccc cgcggcagaa aataatgcc 180
65 aggtcgtact ggataaccgtt actgtaaaaag gcgaccgcca aggcagcaaa atccgtacca 240
66 acatcggttac gctgcaacaa aaagacgaaa gcaccgcaac cgatatgcgc gaactcttaa 300
67 aagaagagcc gtccatcgat ttgcggcgcg gcaacggcac gtcccaattc ctgacgctgc 360
68 gcggcatggg tcagaactct gtcgacatca aggtggacaa cgctattcc gacagccaaa 420
69 tcctttacca ccaaggcaga tttattgtcg atcccgtttt ggtaaagtgc gtttccgtac 480
70 aaaaaggcgc gggttccgcc tctgccggtg tcggcgcgac caacggcgcg atcatcgcca 540
71 aaaccgtcga tgcccaagac ctgctcaaag gcttggataa aaactggggc gtgcgcctca 600
72 acagcggctt tgccagcaac gaaggcgtaa gctacggcgc aagcgtattc ggaaaagagg 660
73 gcaacttcga cggcttggtt tcttacaacc gcaacgatga aaaagattac gaagccggca 720
74 aaggtttccg caatgtcaac ggcggcacaaa ccgtaccgta cagcgcgctg gacaaacgca 780
75 gctacctcgc caaaatcgga acaaccttcg gcgacgacga ccaccgcac gtgttgagcc 840
76 acatgaaaga ccaacaccgg ggcatccgca ctgtgcgtga agaatttacc gtcggcgaca 900
77 aaagtccacg gataaatatt gaccgccaag cccctgttta ccgcgaaact acccaatcca 960
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80 atgtaaaagg ccccaaccat acccgaatca cactcgtgg tgcgaacttc aacttcgaca 1140
81 gccgccttgc cgaacaaacc ctgttgaaat acggtatcaa ctaccgccat caggaaatca 1200
82 aaccgcaagc atttttgaac tcgaaattct ccatcccgac gacagaagag aaaaacggtc 1260
83 aaaaagtcca taaaccgatg gaacaacaaa tgaaagaccg tgcagatgaa gacactgttc 1320
84 acgcctacaa actttccaac ccgacaaaaa ccgataccgg cgtatatgtt gaagccattc 1380
85 acgacatcgg cgatttcacg ctgaccggcg ggctgcgtta cgaccgcttc aagggtgaaa 1440
86 cccatgacgg caaaaccgtt tcaagcagca accttaacct gagtttcggt gtgatttggc 1500
87 agccgcacga aacttgagc ttcagcgca gccacaacta cgccagccgc agcccgcgcc 1560
88 tgtatgacgc gctgcaaacc caggttaaac gcggcacat ctcgattgcc gacggcaca 1620
89 aagccgaacg cgcgcgcaat accgaaatcg gcttcaact caacgacggc acgtttgccg 1680
90 caaacggcag ctacttcttg cagaccatca aagacgcgct tgccaatccg caaaaccgcc 1740
91 acgactctgt cgccgtccgt gaagccgtca atgccgggta catcaaaaac cacggttacg 1800
92 aattgggcgc gtcctaccgc accggcggcc tgactgcaa agtcggcgct agccacagca 1860
93 aaccgcgctt ttacgatacg cacaagaca agctgttgag cgcaatcct gaatttggcg 1920
94 cacaagtcgg ccgcaacttg acggcctccc ttgcctaccg cttccaaaat ccgaatctgg 1980
95 aaatcggtcg gcgcggccgt tatgttcaaa aagctacggg ttcgatattg gcggcaggtc 2040
96 aaaaagaccg caaaggcaac ttggaaaacg ttgtacgcaa aggtttcggt gtgaacgatg 2100
97 tcttcgcaa ctggaaccg ctgggcaaag acacgtcaa tgtcaatctt tcggttaaca 2160
98 acgtgttcaa caagttctac tatccgcaca gccaacgctg gaccaatacc ctgccggcg 2220
99 tgggacgtga tgtacgcttg ggcgtgaact acaagttcta aaacgcacat cccgaaaaaa 2280
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102 &lt;210&gt; SEQ ID NO: 4

103 &lt;211&gt; LENGTH: 720

104 &lt;212&gt; TYPE: PRT

105 &lt;213&gt; ORGANISM: Neisseria meningitidis

107 &lt;400&gt; SEQUENCE: 4

108 Met Asn Thr Pro Leu Phe Arg Leu Ser Leu Leu Ser Leu Thr Leu Ala

109 1 5 10 15

110 Ala Gly Phe Ala His Ala Ala Glu Asn Asn Ala Lys Val Val Leu Asp

111 20 25 30

112 Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn

113 35 40 45

114 Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg

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115	50					55					60					
116	Glu	Leu	Leu	Lys	Glu	Glu	Pro	Ser	Ile	Asp	Phe	Gly	Gly	Gly	Asn	Gly
117	65					70					75					80
118	Thr	Ser	Gln	Phe	Leu	Thr	Leu	Arg	Gly	Met	Gly	Gln	Asn	Ser	Val	Asp
119					85					90					95	
120	Ile	Lys	Val	Asp	Asn	Ala	Tyr	Ser	Asp	Ser	Gln	Ile	Leu	Tyr	His	Gln
121				100					105					110		
122	Gly	Arg	Phe	Ile	Val	Asp	Pro	Ala	Leu	Val	Lys	Val	Val	Ser	Val	Gln
123			115					120					125			
124	Lys	Gly	Ala	Gly	Ser	Ala	Ser	Ala	Gly	Ile	Gly	Ala	Thr	Asn	Gly	Ala
125		130					135					140				
126	Ile	Ile	Ala	Lys	Thr	Val	Asp	Ala	Gln	Asp	Leu	Leu	Lys	Gly	Leu	Asp
127	145					150					155					160
128	Lys	Asn	Trp	Gly	Val	Arg	Leu	Asn	Ser	Gly	Phe	Ala	Ser	Asn	Glu	Gly
129					165					170					175	
130	Val	Ser	Tyr	Gly	Ala	Ser	Val	Phe	Gly	Lys	Glu	Gly	Asn	Phe	Asp	Gly
131				180					185					190		
132	Leu	Phe	Ser	Tyr	Asn	Arg	Asn	Asp	Glu	Lys	Asp	Tyr	Glu	Ala	Gly	Lys
133			195					200					205			
134	Gly	Phe	Arg	Asn	Val	Asn	Gly	Gly	Lys	Thr	Val	Pro	Tyr	Ser	Ala	Leu
135		210					215					220				
136	Asp	Lys	Arg	Ser	Tyr	Leu	Ala	Lys	Ile	Gly	Thr	Thr	Phe	Gly	Asp	Asp
137	225					230					235					240
138	Asp	His	Arg	Ile	Val	Leu	Ser	His	Met	Lys	Asp	Gln	His	Arg	Gly	Ile
139					245					250					255	
140	Arg	Thr	Val	Arg	Glu	Glu	Phe	Thr	Val	Gly	Asp	Lys	Ser	Ser	Arg	Ile
141				260					265						270	
142	Asn	Ile	Asp	Arg	Gln	Ala	Pro	Ala	Tyr	Arg	Glu	Thr	Thr	Gln	Ser	Asn
143			275					280						285		
144	Thr	Asn	Leu	Ala	Tyr	Thr	Gly	Lys	Asn	Leu	Gly	Phe	Val	Glu	Lys	Leu
145		290					295					300				
146	Asp	Ala	Asn	Ala	Tyr	Val	Leu	Glu	Lys	Glu	Arg	Tyr	Ser	Ala	Asp	Asp
147	305					310					315					320
148	Ser	Gly	Thr	Gly	Tyr	Ala	Gly	Asn	Val	Lys	Gly	Pro	Asn	His	Thr	Arg
149					325						330				335	
150	Ile	Thr	Thr	Arg	Gly	Ala	Asn	Phe	Asn	Phe	Asp	Ser	Arg	Leu	Ala	Glu
151				340						345					350	
152	Gln	Thr	Leu	Leu	Lys	Tyr	Gly	Ile	Asn	Tyr	Arg	His	Gln	Glu	Ile	Lys
153			355						360					365		
154	Pro	Gln	Ala	Phe	Leu	Asn	Ser	Lys	Phe	Ser	Ile	Pro	Thr	Thr	Glu	Glu
155		370					375					380				
156	Lys	Asn	Gly	G												

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164 His Asp Gly Lys Thr Val Ser Ser Ser Asn Leu Asn Pro Ser Phe Gly
165      450      455      460
166 Val Ile Trp Gln Pro His Glu His Trp Ser Phe Ser Ala Ser His Asn
167 465      470      475      480
168 Tyr Ala Ser Arg Ser Pro Arg Leu Tyr Asp Ala Leu Gln Thr His Gly
169      485      490      495
170 Lys Arg Gly Ile Ser Ile Ala Asp Gly Thr Lys Ala Glu Arg Ala
171      500      505      510
172 Arg Asn Thr Glu Ile Gly Phe Asn Tyr Asn Asp Gly Thr Phe Ala Ala
173      515      520      525
174 Asn Gly Ser Tyr Phe Trp Gln Thr Ile Lys Asp Ala Leu Ala Asn Pro
175      530      535      540
176 Gln Asn Arg His Asp Ser Val Ala Val Arg Glu Ala Val Asn Ala Gly
177 545      550      555      560
178 Tyr Ile Lys Asn His Gly Tyr Glu Leu Gly Ala Ser Tyr Arg Thr Gly
179      565      570      575
180 Gly Leu Thr Ala Lys Val Gly Val Ser His Ser Lys Pro Arg Phe Tyr
181      580      585      590
182 Asp Thr His Lys Asp Lys Leu Leu Ser Ala Asn Pro Glu Phe Gly Ala
183      595      600      605
184 Gln Val Gly Arg Thr Trp Thr Ala Ser Leu Ala Tyr Arg Phe Gln Asn
185      610      615      620
186 Pro Asn Leu Glu Ile Gly Trp Arg Gly Arg Tyr Val Gln Lys Ala Thr
187 625      630      635      640
188 Gly Ser Ile Leu Ala Ala Gly Gln Lys Asp Arg Lys Gly Asn Leu Glu
189      645      650      655
190 Asn Val Val Arg Lys Gly Phe Gly Val Asn Asp Val Phe Ala Asn Trp
191      660      665      670
192 Lys Pro Leu Gly Lys Asp Thr Leu Asn Val Asn Leu Ser Val Asn Asn
193      675      680      685
194 Val Phe Asn Lys Phe Tyr Tyr Pro His Ser Gln Arg Trp Thr Asn Thr
195      690      695      700
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200 <210> SEQ ID NO: 5
201 <211> LENGTH: 2600
202 <212> TYPE: DNA
203 <213> ORGANISM: Neisseria gonorrhoeae
205 <400> SEQUENCE: 5
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207 caccgagtga atcggttccg tactatttgt actgtctgcg gcttcgccgc cttgtcctga 120
208 tttttgttag tccacatata catttccgac aaaacctgtc aacaaaaaac aacgcttcgc 180
209 aaataaaaaac gataatcagc tttacacaac cccccccgc taatataaac aaaaataatt 240
210 attattattt tttcttatcc tgccaaacct taacggtttg gcttaacttc cttcataca 300
211 ctcaaaagga cgaacaaatg aacgccccgt ttttcgcct cagcctgctc tcgctcacac 360
212 ttgccgccgg ctttgccac gcggcagaaa ataatgcaa tgtcgcttg gataccgtta 420
213 ccgtaaaagg cgaccgcaa ggcagcaaaa tccgtaccaa catcgttacg cttcaacaaa 480
214 aagacgaaag caccgcaacc gatatgcgcg aactcttaaa agaagagccc tccatcgatt 540
215 tcggcgccgg caacggcacg tcccaattcc tgacgctgcg cggtatgggt cagaactctg 600

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216 tcgacatcaa ggtggacaac gcctattccg acagccaaat cctttaccac caaggcagat 660
217 ttattgtcga tcccgctttg gttaaagtcg tttccgtaca gaaaggcgcg gggtccgcct 720
218 ctgccggtat cggcgcgacc aacggcgcgga tcatcgccaa aaccgctcgat gcccaagacc 780
219 tgctcaaagg cttggataaa aactggggcg tgcgcctcaa cagcggtctt gccggcaaca 840
220 acggcgcaag ctacggcgca agcgtattcg gaaaagaggg caacttcgac ggtttgttct 900
221 cttacaaccg caacgatgaa aaagattacg aagccggcaa aggtttccgc aatgacaacg 960
222 gcggcaaaac cgtaccgtac agcgcgctgg acaaacgcag ctacctcgcc aaaatcggaa 1020
223 caaccttcgg cgacggcgac caccgcatcg tggtgagcca tatgaaagac caacaccggg 1080
224 gcatccgcac tgtgcgtgaa gagtttgccg tcagcgaaaa aaattcacgg ataactatta 1140
225 aacgccaaag cccatcctac cgcgaaacca ctcaatccaa caccaacttg cgtacaccg 1200
226 gcaaagattt gggctttgtc gaaaaactgg atgccaacgc ctatgtgttg gaaaagaaac 1260
227 gctattccgc cgatgacaaa gataacggct acgcaggcaa tgtaaaaggc cccaaccata 1320
228 cccgaatcgc cactcggagt atgaacttca acttcgacag ccgccttgcc gaacaaaccc 1380
229 tgttgaaata cggcatcaac taccgccatc aggaaatcaa accgcaagcg tttttgaact 1440
230 cgggaatttg aataaaagat aaagaaaaag caactaatga agagaaaaag aagaaccgtg 1500
231 aaaatgaaaa aattgccaaa gcctaccgcc tgaccaaccc gaccaaacc gataccggcg 1560
232 cgtatatcga agccattcac gagattgacg gctttaccct gaccggcggg ctgcgttacg 1620
233 accgcttcaa ggtgaaaacc caccgacgga aaaccgtttc aagcagcagc ctcaaccga 1680
234 gtttcggcgt gatttggcag ccgcgcgaac actggagctt cagcgcgagc cacaactacg 1740
235 ccggccgcag ccgcgcctg tatgacgctc tgcaaaccga cggcaagcgc ggcacatct 1800
236 cgattgccga cggcacgaaa gccgaacgcg cgcgcaatac cgaaatcggc ttcaactaca 1860
237 acgacggcac gtttgccgca aacggcagct acttcgggca gaccatcaaa gacgcgcttg 1920
238 ccaatccgca aaaccgccac gactccgtcg ccgtccgcga agccgtcaac gccggctaca 1980
239 tcaaaaaaca cggttacgaa ttgggcgcgt cctaccgcac cggcggcctg accgcaaag 2040
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241 cgaaccctga atttggcgca caagtcggcc gcacttggac ggcctccctt gcctaccgct 2160
242 tcaaaaaacc gaatctggaa atcggctggc gcggtcgtta tgttcaaaaa gccgtgggtt 2220
243 cgatattggc ggcaggtcaa aaagaccgcg acggcaaatt ggaaaacggt gtacgccaaag 2280
244 gtttcggtgt gaacgatgtc ttcgccaaact ggaaaaccgt gggcaaagac acgctcaatg 2340
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246 ccaataccct gccgggcgtg ggacgtgatg tacgcctggg cgtgaactac aagttctaaa 2460
247 acgcacatcc cgaaaaaatg ccgtctgaaa gcctttcaga cggcatctgt cctgataatt 2520
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251 <210> SEQ ID NO: 6
252 <211> LENGTH: 713
253 <212> TYPE: PRT
254 <213> ORGANISM: Neisseria gonorrhoeae
256 <400> SEQUENCE: 6
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260 20 25 30
261 Thr Val Thr Val Lys Gly Asp Arg Gln Gly Ser Lys Ile Arg Thr Asn
262 35 40 45
263 Ile Val Thr Leu Gln Gln Lys Asp Glu Ser Thr Ala Thr Asp Met Arg
264 50 55 60
265 Glu Leu Leu Lys Glu Glu Pro Ser Ile Asp Phe Gly Gly Gly Asn Gly
266 65 70 75 80

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 2,5,9

Seq#:22; Xaa Pos. 2,5,9

**VERIFICATION SUMMARY**

DATE: 03/09/2005

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L:19 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:752 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:756 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21  
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:769 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:773 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22  
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0